



IFWO

## RAW SEQUENCE LISTING

DATE: 09/21/2004

PATENT APPLICATION: US/10/822,613

TIME: 16:37:37

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09212004\J822613.raw

3 &lt;110&gt; APPLICANT: SCARPACE, PHILIP J.

4 LI, GANG

6 &lt;120&gt; TITLE OF INVENTION: RAAV VECTOR-BASED PRO-OPIOMELANOCORTIN COMPOSITIONS AND

## METHODS

7 OF USE

9 &lt;130&gt; FILE REFERENCE: 4300.015400

C--&gt; 11 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/822,613

C--&gt; 11 &lt;141&gt; CURRENT FILING DATE: 2004-04-12

11 &lt;150&gt; PRIOR APPLICATION NUMBER: 60/462,496

12 &lt;151&gt; PRIOR FILING DATE: 2003-04-11

14 &lt;160&gt; NUMBER OF SEQ ID NOS: 54

16 &lt;170&gt; SOFTWARE: PatentIn version 3.2

18 &lt;210&gt; SEQ ID NO: 1

19 &lt;211&gt; LENGTH: 804

20 &lt;212&gt; TYPE: DNA

21 &lt;213&gt; ORGANISM: Homo sapiens

23 &lt;400&gt; SEQUENCE: 1

24 atgccgagat cgtgctgcag ccgctcgggg gccctgttgc tggccttgc gcttcaggcc 60  
 26 tccatggaag tgcgtggctg gtgcctggag agcagccagt gtcaggacct caccacgga 120  
 28 agcaacctgc tggagtgcac ccgggacctg aagcccgacc tctcgccga gactcccatg 180  
 30 ttcccgggaa atggcgacga gcagcctctg accgagaacc cccggaagta cgtcatgggc 240  
 32 cacttccgct gggaccgatt cggccgcgc aacagcagca gcagcggcag cagcggcgca 300  
 34 gggcagaagc gcgaggacgt ctcagcgggc gaagactgcg gcccgctgcc tgagggcggc 360  
 36 cccgagcccc gcagcgatgg tgccaagcgc gggccgcgcg agggcaagcg ctcctactcc 420  
 38 atggagcact tccgctgggg caagccgggtg ggcaagaagc ggcgccagc gaaggtgtac 480  
 40 cctaacggcg ccgaggacga gtgcggccag gccctcccc tggagttaa gaggagctg 540  
 42 actggccagc gactccggga gggagatggc cccgacggcc ctgccgatga cggcgccagg 600  
 44 gccagggccg acctggagca cagcctgctg gtggcgggcc agaagaagga cgagggcccc 660  
 46 tacaggatgg agcacttccg ctggggcagc ccgcccagg acaagcgcta cggcggtttc 720  
 48 atgacctccg agaagagcca gacgcccctg gtgacgctgt tcaaaaacgc catcatcaag 780  
 50 aacgcctaca agaaggcgca gtga 804

53 &lt;210&gt; SEQ ID NO: 2

54 &lt;211&gt; LENGTH: 267

55 &lt;212&gt; TYPE: PRT

56 &lt;213&gt; ORGANISM: Homo sapiens

58 &lt;400&gt; SEQUENCE: 2

60 Met Pro Arg Ser Cys Cys Ser Arg Ser Gly Ala Leu Leu Leu Ala Leu  
 61 1 5 10 15  
 64 Leu Leu Gln Ala Ser Met Glu Val Arg Gly Trp Cys Leu Glu Ser Ser  
 65 20 25 30  
 68 Gln Cys Gln Asp Leu Thr Thr Glu Ser Asn Leu Leu Glu Cys Ile Arg  
 69 35 40 45  
 72 Ala Cys Lys Pro Asp Leu Ser Ala Glu Thr Pro Met Phe Pro Gly Asn  
 73 50 55 60

(pg. 6)

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76 Gly Asp Glu Gln Pro Leu Thr Glu Asn Pro Arg Lys Tyr Val Met Gly
77 65          70          75          80
80 His Phe Arg Trp Asp Arg Phe Gly Arg Arg Asn Ser Ser Ser Ser Gly
81          85          90          95
84 Ser Ser Gly Ala Gly Gln Lys Arg Glu Asp Val Ser Ala Gly Glu Asp
85          100          105          110
88 Cys Gly Pro Leu Pro Glu Gly Gly Pro Glu Pro Arg Ser Asp Gly Ala
89          115          120          125
92 Lys Pro Gly Pro Arg Glu Gly Lys Arg Ser Tyr Ser Met Glu His Phe
93          130          135          140
96 Arg Trp Gly Lys Pro Val Gly Lys Lys Arg Arg Pro Val Lys Val Tyr
97 145          150          155          160
100 Pro Asn Gly Ala Glu Asp Glu Ser Ala Glu Ala Phe Pro Leu Glu Phe
101          165          170          175
104 Lys Arg Glu Leu Thr Gly Gln Arg Leu Arg Glu Gly Asp Gly Pro Asp
105          180          185          190
108 Gly Pro Ala Asp Asp Gly Ala Gly Ala Gln Ala Asp Leu Glu His Ser
109          195          200          205
112 Leu Leu Val Ala Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu
113          210          215          220
116 His Phe Arg Trp Gly Ser Pro Pro Lys Asp Lys Arg Tyr Gly Gly Phe
117 225          230          235          240
120 Met Thr Ser Glu Lys Ser Gln Thr Pro Leu Val Thr Leu Phe Lys Asn
121          245          250          255
124 Ala Ile Ile Lys Asn Ala Tyr Lys Lys Gly Glu
125          260          265
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 559
130 <212> TYPE: DNA
131 <213> ORGANISM: Gorilla gorilla
133 <400> SEQUENCE: 3
134 ctcgcccgag actcccatgt tcccgggcaa tggcgacgag cagcctctga ccgagaaccc 60
136 ccggaagtac gtcattgggccc acttccgctg ggaccgattc ggccgccgca acagcagcag 120
138 cagcagcggc agcggcgagc ggcagaagcg cgaggatgtc tcagcgggag aagaccgcgg 180
140 cccgctgcct gagggcgggc cccagccccc cagtgatgtt gccaaagccg gcccgcgaga 240
142 gggcaagcgc tctactcca tggagcactt ccgctggggc aagccggtgg gcaagaagcg 300
144 gcgcccgggt aaggtgtacc ctaacggcgc cgaggacgag tcggccgagg ccttccccct 360
146 ggagtccaag agggagctga ctggccagcg accccgggag ggagatggcc ccgacggccc 420
148 tgccgatgac ggcgcggggg cccaggccga cctggagcat agcctgctgg tggcggccga 480
150 gaagaaggac gagggccccct acgggatgga gcacttccgc tggggcagcc cgcccaagga 540
152 caagcgctac ggcgggtttc
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 186
157 <212> TYPE: PRT
158 <213> ORGANISM: Gorilla gorilla
160 <400> SEQUENCE: 4
162 Ser Ala Glu Thr Pro Met Phe Pro Gly Asn Gly Asp Glu Gln Pro Leu
163 1          5          10          15
166 Thr Glu Asn Pro Arg Lys Tyr Val Met Gly His Phe Arg Trp Asp Arg

```

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```

167          20          25          30
170 Phe Gly Arg Arg Asn Ser Ser Ser Ser Ser Gly Ser Gly Ala Gly Gln
171          35          40          45
174 Lys Arg Glu Asp Val Ser Ala Gly Glu Asp Arg Gly Pro Leu Pro Glu
175          50          55          60
178 Gly Gly Pro Glu Pro Arg Ser Asp Gly Ala Lys Pro Gly Pro Arg Glu
179 65          70          75          80
182 Gly Lys Arg Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val
183          85          90          95
186 Gly Lys Lys Arg Arg Pro Val Lys Val Tyr Pro Asn Gly Ala Glu Asp
187          100          105          110
190 Glu Ser Ala Glu Ala Phe Pro Leu Glu Phe Lys Arg Glu Leu Thr Gly
191          115          120          125
194 Gln Arg Pro Arg Glu Gly Asp Gly Pro Asp Gly Pro Ala Asp Asp Gly
195          130          135          140
198 Ala Gly Ala Gln Ala Asp Leu Glu His Ser Leu Leu Val Ala Ala Glu
199 145          150          155          160
202 Lys Lys Asp Glu Gly Pro Tyr Gly Met Glu His Phe Arg Trp Gly Ser
203          165          170          175
206 Pro Pro Lys Asp Lys Arg Tyr Gly Gly Phe
207          180          185
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 795
212 <212> TYPE: DNA
213 <213> ORGANISM: Macaca nemestrina
215 <400> SEQUENCE: 5
216 atgccgagat cgtgctgcag ccgctcgggg gccctgttgc tggccttgct gcttcaggcc 60
218 tccatggaag tgcgtggctg gtgcctggag agcagccagt gtcaggacct caccacggaa 120
220 agcaacctgc tggagtgcac ccgggcctgc aagcccgcac ttccggccga gactccggtg 180
222 ttcccgggca atggcgagca gcagcctctg accgagaacc ccggaagta cgtcatgggc 240
224 cacttccgct gggaccgatt cggccgcgc aacagtagca gcggcagcgc gcaccagaag 300
226 cgcgaggacg tcgcggctgg cgaagaccgc ggccctgtac ctgagggtgg ccccgagccc 360
228 cgtggcgatg gcgcggggcc gggccgcgc gagggcaagc gtcctactc catggagcac 420
230 ttccgctggg gcaagccggt gggcaagaag cggcgcccgg tgaaggtgta cccaatggc 480
232 gccgaggacg agtcggccga ggccctcccc ctggagttca agaggagct gaccggccag 540
234 cggccccggg cgggggatgg ccccgatggc cctgccgacg acggcgcggg gccccgggcc 600
236 gacctggagc acagcctgct ggtggcgggc gagaagaagg atgagggcc ctacaggatg 660
238 gagcacttcc gctggggcag cccgcccagg gacaagcgct acggcggtt catgacctcc 720
240 gagaagagcc agactcccct ggtgacactg ttcaaaaacg ccatcatcaa gaacgcctac 780
242 aagaagggcc agtga 795
245 <210> SEQ ID NO: 6
246 <211> LENGTH: 264
247 <212> TYPE: PRT
248 <213> ORGANISM: Macaca nemestrina
250 <400> SEQUENCE: 6
252 Met Pro Arg Ser Cys Cys Ser Arg Ser Gly Ala Leu Leu Leu Ala Leu
253 1          5          10          15
256 Leu Leu Gln Ala Ser Met Glu Val Arg Gly Trp Cys Leu Glu Ser Ser
257          20          25          30

```

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```

260 Gln Cys Gln Asp Leu Thr Thr Glu Ser Asn Leu Leu Glu Cys Ile Arg
261          35                      40                      45
264 Ala Cys Lys Pro Asp Leu Ser Ala Glu Thr Pro Val Phe Pro Gly Asn
265          50                      55                      60
268 Gly Asp Glu Gln Pro Leu Thr Glu Asn Pro Arg Lys Tyr Val Met Gly
269 65                      70                      75                      80
272 His Phe Arg Trp Asp Arg Phe Gly Arg Arg Asn Ser Ser Ser Gly Ser
273          85                      90                      95
276 Ala His Gln Lys Arg Glu Asp Val Ala Ala Gly Glu Asp Arg Gly Leu
277          100                     105                     110
280 Leu Pro Glu Gly Gly Pro Glu Pro Arg Gly Asp Gly Ala Gly Pro Gly
281          115                     120                     125
284 Pro Arg Glu Gly Lys Arg Ser Tyr Ser Met Glu His Phe Arg Trp Gly
285          130                     135                     140
288 Lys Pro Val Gly Lys Lys Arg Arg Pro Val Lys Val Tyr Pro Asn Gly
289 145                     150                     155                     160
292 Ala Glu Asp Glu Ser Ala Glu Ala Phe Pro Leu Glu Phe Lys Arg Glu
293          165                     170                     175
296 Leu Thr Gly Gln Arg Pro Arg Ala Gly Asp Gly Pro Asp Gly Pro Ala
297          180                     185                     190
300 Asp Asp Gly Ala Gly Pro Arg Ala Asp Leu Glu His Ser Leu Leu Val
301          195                     200                     205
304 Ala Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg
305          210                     215                     220
308 Trp Gly Ser Pro Pro Lys Asp Lys Arg Tyr Gly Gly Phe Met Thr Ser
309 225                     230                     235                     240
312 Glu Lys Ser Gln Thr Pro Leu Val Thr Leu Phe Lys Asn Ala Ile Ile
313          245                     250                     255
316 Lys Asn Ala Tyr Lys Lys Gly Gln
317          260
320 <210> SEQ ID NO: 7
321 <211> LENGTH: 496
322 <212> TYPE: DNA
323 <213> ORGANISM: Pongo pygmaeus
325 <400> SEQUENCE: 7
326 gaagtacgtc atgggccact tccgctggga ccgatttggc cgccgcaaca gcagcagcgg      60
328 cagcggtagc ggcgcagggc agaagcgcgga ggacgtcgca gcgggcgaag accgcggccc      120
330 actgcctgag ggcgcccccg agccccgcag cgatggcgcc gagccgggccc cgcgcgaggg      180
332 caagegctcc tactccatgg agcacttccg ctggggcaag ccggtgggca agaagcggcg      240
334 cccggtgaag gtgtacccca acggcgccga ggacgagtcg gccgaggcct tccccctgga      300
336 gttcaagagg gagccgaccg gccagcggct ccgggaggga gatggccccg acggccctgc      360
338 cgatgacggc gccggggccc gggccgacct ggagcacaac ctgctggtgg cggccgagaa      420
340 gaaggacgag ggcccctaca ggatggagca cttccgctgg ggcagcccgc ccaaggacaa      480
342 gcgctacggc ggtttc
345 <210> SEQ ID NO: 8
346 <211> LENGTH: 165
347 <212> TYPE: PRT
348 <213> ORGANISM: Pongo pygmaeus
350 <400> SEQUENCE: 8

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```

352 Lys Tyr Val Met Gly His Phe Arg Trp Asp Arg Phe Gly Arg Arg Asn
353 1          5          10          15
356 Ser Ser Ser Gly Ser Gly Ser Gly Ala Gly Gln Lys Arg Glu Asp Val
357          20          25          30
360 Ala Ala Gly Glu Asp Arg Gly Pro Leu Pro Glu Gly Gly Pro Glu Pro
361          35          40          45
364 Arg Ser Asp Gly Ala Glu Pro Gly Pro Arg Glu Gly Lys Arg Ser Tyr
365          50          55          60
368 Ser Met Glu His Phe Arg Trp Gly Lys Pro Val Gly Lys Lys Arg Arg
369 65          70          75          80
372 Pro Val Lys Val Tyr Pro Asn Gly Ala Glu Asp Glu Ser Ala Glu Ala
373          85          90          95
376 Phe Pro Leu Glu Phe Lys Arg Glu Pro Thr Gly Gln Arg Leu Arg Glu
377          100         105         110
380 Gly Asp Gly Pro Asp Gly Pro Ala Asp Asp Gly Ala Gly Ala Arg Ala
381          115         120         125
384 Asp Leu Glu His Asn Leu Leu Val Ala Ala Glu Lys Lys Asp Glu Gly
385          130         135         140
388 Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp Lys
389 145         150         155         160
392 Arg Tyr Gly Gly Phe
393          165

```

396 &lt;210&gt; SEQ ID NO: 9

397 &lt;211&gt; LENGTH: 804

398 &lt;212&gt; TYPE: DNA

399 &lt;213&gt; ORGANISM: Sus scroffa

401 &lt;400&gt; SEQUENCE: 9

```

402 atgccgagat tgtgcggcag tcgctcgggg gccctgctgc tgaccttgct gctccaggcc 60
404 tccatgggag tgcgcggctg gtgcttgagg agcagccagt gtcaggacct ctccacggaa 120
406 agtaacttgt tggcgtgcat ccgggcctgc aaaccagatc tctctgcgga gacgccctg 180
408 tttcccgga acggcgacgc gcaaccgctg accgagaacc cccggaagta cgtcatgggc 240
410 cacttccgct gggaccgctt cggccgcggg aatggcagca gcagcggcgg cggtggcgg 300
412 ggcggcgggc cgggccagaa gcgcgaggag gaggaggagg cggcgggcga aggcccggg 360
414 ccccgcgagg atggcgctgc gccggggccc cgccaggaca agcgctccta ctccatggag 420
416 cacttccgct ggggcaagcc cgtgggcaag aagcggcgcc cggggaaggt gtatcccaac 480
418 ggcgcggagg acgagttggc cgaggccttc cccctcgagt tcaggaggga gctggccggg 540
420 gcgccccccg agccggcacg ggaccccgag gcccgggccg agggcgcggc cgccccggcc 600
422 gagctggagt acgggctggt ggccgaggcc gaggcggccg agaagaagga cgaagggccc 660
424 tataagatgg agcacttccg ctggggcagc ccgccaagg acaagcgcta cggcggcttc 720
426 atgacctccg agaagagcca gacgcccctg gtcacgctgt tcaaaaacgc catcgtcaag 780
428 aacgcccaca agaagggcca gtga 804

```

431 &lt;210&gt; SEQ ID NO: 10

432 &lt;211&gt; LENGTH: 267

433 &lt;212&gt; TYPE: PRT

434 &lt;213&gt; ORGANISM: Sus scroffa

436 &lt;400&gt; SEQUENCE: 10

```

438 Met Pro Arg Leu Cys Gly Ser Arg Ser Gly Ala Leu Leu Leu Thr Leu
439 1          5          10          15
442 Leu Leu Gln Ala Ser Met Gly Val Arg Gly Trp Cys Leu Glu Ser Ser

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/822,613

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Input Set : A:\Sequence Listing.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; Xaa Pos. 174  
Seq#:32; Xaa Pos. 184  
Seq#:33; Xaa Pos. 120,121  
Seq#:37; Xaa Pos. 129

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:41,42,43,44,45,46,47,48,49,50,51,52,53,54

**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:160

L:1658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:176

L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:112

L:2021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:128